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AB Random amplified polymorphic DNA (RAPD) techniques were employed to estimated the genetic diversity within 13 varieties of Chinese, 26 varieties of Japanese and 11 varieties of Korean, European and Canadian B. napus. A similarity matrix was calculated from 181 polymorphic bands that were amplified with 21 strictly selected PCR primers. Based on the matrix, a phenogram was drawn using the neighbor-joining method, and **principal component** analysis (PCA) was also carried out with the data of the polymorphic bands. These two analyses enabled to identify a correlation among the varieties and 43 out of 50 varieties were clustered into three major groups. Most of the Japanese and four out of the 13 Chinese cultivars were clustered into one of the three major groups whereas most of the Chinese varieties were not included in the three major groups. European spring and winter types were clustered into two different groups and some of the Asian varieties were included in the groups. Our results also indicate that most of the Chinese and Japanese B. napus varieties in this study showed a unique genetic background that separated them from European varieties.

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TI Data visualization and analysis tools for high density microarrays.
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AB Microarrays provide the opportunity to study **gene expression** patterns on a genomic scale. Thousands of genes are arrayed on a microscope slide and relative expression levels are determined by measuring fluorescence intensity of labeled mRNA hybridized to the arrays. We have developed a package of Java based tools to facilitate the analysis of this data, allowing the user to display graphical representations of hybridized slides, perform statistical tests to identify differentially expressed or similar genes, and view and export the results. Expression data is read from flat files or a relational database, via JDBC, as single slides or a series of experiments. A representation of the hybridizations is generated, showing a grid of experiments and genes, where multiple experiments can easily be compared with each other. A detail view focusing on a single slide is available, showing each spot as a rectangle in its appropriate location on the slide. In both displays, elements are colored to represent relative expression, based on several options including two split-ratio displays, green/red overlay and false color. Clicking on an element will allow the user to access information about the underlying gene. Fluorescence intensities can be normalized using a number of strategies. Differentially expressed genes can be identified using a variety of statistical tests. Several types of gene and experiment analyses have been facilitated, including hierarchical and K-means clustering, self-organizing maps, **principal component** analysis and support vector